



5/7

M <sub>110</sub> (1-38)peptide	26	...PPVV <u>K</u> <u>R</u> <u>Q</u> <u>K</u> <u>T</u> <u>K</u> <u>V</u> <u>K</u> <u>F</u>	38 SEQ ID. NO: 3
G <sub>L</sub>	52	...TVQ <u>E</u> <u>K</u> <u>K</u> <u>V</u> <u>K</u> <u>R</u> <u>V</u> <u>S</u> <u>E</u> <u>F</u> <u>A</u> <u>D</u> <u>Q</u> <u>G</u> <u>L</u> ...	69 SEQ ID. NO: 4
G <sub>M</sub> (63-93)peptide	63	G <u>R</u> <u>R</u> <u>V</u> <u>S</u> <u>E</u> <u>F</u> <u>A</u> <u>D</u> <u>N</u> <u>E</u> <u>G</u> ...	73 SEQ ID. NO: 5

*Fig. 5*



6/7

G <sub>L</sub>	132	VCLE---NCVLKEKAIAGTVKVQNLAFEKVVKIRM---TFDTWKSFT	172 SEQ ID. NO: 6
R5	157	VCLE---NCSLQERTVTGTVKVKNVSEFKKVOIRI---TFDSWKNYT	197 SEQ ID. NO: 7
R6	177	VCLE---RVTCSDLGISGTVRVCNVAFEKQVAVRY---TFSGWRSTH	217 SEQ ID. NO: 8
G <sub>M</sub>	128	AILES-TESSLGSTSITKGIIRVLNVSEFKLVYVRM---SLDDWQTHY	170 SEQ ID. NO: 9
GAC1	244	VKLHSLTQLGDDSSKITGLVYVKNLSFEKYLEIKF---TFNSWRDIH	287 SEQ ID. NO: 10
AMYL	33	VQLDS---YNYDGSTFSGKIYVKNIAYSKKVTVIYADGSDNWNNG	75 SEQ ID. NO: 11
Consensus		φ.G.V.V.Nφ.F.K.V.V.φ.....W I Y L I	
PHOS	398	RHLQIIYEINQRFILNRVAAAFPGDVDRLRRMS ** *** *	429 SEQ ID. NO: 12
G <sub>L</sub>	173	DFPCQYVKDITYAGSDRDTESEDISLPEKIQSYE-----	205
R5	198	DVDCVYMKNVYGGTSDTFSEFAIDLPPVIPTEQ-----	230
R6	218	EAVARWRGPAGPEGTEDVFTEGFPVPPFILLEIGS-----	251
G <sub>M</sub>	171	DILAEYVPNSCDG-ETDQFSEKIVLVPPYQKDG-----	203
GAC1	288	YVTANFNRTIN--SNVDEFKETIDLNSLKYILLIKRIITMERNTSS	331
AMYL	76	NTIAASYSAPISGSNYEYWTFSASINGIK-----	104
Consensus		D.F.F...φ E W	
PHOS	330	LVEEGAVK * * *	437
G <sub>L</sub>	206	---RMEFAVCYECNGQSYWDSNKGKNYRI	231
R5	231	---KIEFCISYHANGQVFDNNDGQNYRI	256
R6	252	---RVHFAVRYQVAGAEYWDNNDHRDYSL	282
G <sub>M</sub>	204	---KVEFCIRYETSVGTFSNNGTNYTF	229
GAC1	332	CPLNIELCCRYDVNNETYYDNNNGKNYHL	360
AMYL	105	-----EFYIKYEVSGKTYDNNNSANYQV	128
Consensus		F.φ.Y.....YW..N....Y.φ L FY	

Fig. 6